

Application
Number

SEARCH

IDS Flag Clearance for Application 10766421

IDS
Information

| Content | Mailroom Date | Entry Number | IDS Review | Reviewer |
|---------|---------------|-----------------|-------------------------------------|-------------------------------|
| M844 | 11-24-2004 | 16 | <input checked="" type="checkbox"/> | 12-16-2004 13:56:16 gtrammell |
| M844 | 01-27-2004 | 21 | <input checked="" type="checkbox"/> | 01-03-2006 07:37:32 YPak |

UPDATE

Message Display



This Action cannot be performed as there is a(n) Prior Art
Filed action waiting for response

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Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % | | Query Match Length | DB | ID | Description |
|---------------|-------|-------|-----------------------|----|----------|--------------------|
| | Score | Match | | | | |
| 1 | 1298 | 100.0 | 254 | 4 | AAB47522 | Aab47522 (R)-2-oct |
| 2 | 944 | 72.7 | 254 | 4 | AAB49773 | Aab49773 Protein w |
| 3 | 586.5 | 45.2 | 257 | 7 | ADF06077 | Adf06077 Bacterial |
| 4 | 582.5 | 44.9 | 248 | 6 | ADB06934 | Adb06934 Alloiococ |
| 5 | 582.5 | 44.9 | 281 | 6 | ADB06936 | Adb06936 Alloiococ |
| 6 | 574.5 | 44.3 | 246 | 8 | ADN17584 | Adn17584 Bacterial |
| 7 | 505.5 | 38.9 | 261 | 6 | ABU29919 | Abu29919 Protein e |
| 8 | 498.5 | 38.4 | 261 | 5 | AAE20115 | Aae20115 Lactobaci |
| 9 | 496.5 | 38.3 | 261 | 9 | ADZ77293 | Adz77293 Bacillus |
| 10 | 495.5 | 38.2 | 261 | 9 | ADZ77291 | Adz77291 Bacillus |
| 11 | 495.5 | 38.2 | 261 | 9 | ADZ77289 | Adz77289 Bacillus |
| 12 | 495.5 | 38.2 | 261 | 9 | ADZ77283 | Adz77283 Bacillus |
| 13 | 494.5 | 38.1 | 261 | 3 | AAy96271 | Aay96271 B. subtil |
| 14 | 494.5 | 38.1 | 261 | 3 | AAy54424 | Aay54424 Amino aci |

RESULT 1

AAB47522

ID AAB47522 standard; protein; 254 AA.

XX

AC AAB47522;

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DT 04-DEC-2001 (first entry)

XX

DE (R)-2-octanol dehydrogenase.

XX

KW (R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme;

KW oxidize; optical isomer; (R)-2-octanol; 4-haloacetoacetate ester;

KW (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor;

KW D-carnitine; (R)-propoxybenzene.

XX

OS *Pichia finlandica*.

XX

PN WO200161014-A1.

XX

PD 23-AUG-2001.

XX

PF 15-FEB-2001; 2001WO-JP001082.

XX

PR 16-FEB-2000; 2000JP-00043506.

PR 08-DEC-2000; 2000JP-00374593.

XX

PA (DAIL) DAICEL CHEM IND LTD.

XX

PI Kudoh M, Yamamoto H;

XX

DR WPI; 2001-596701/67.

DR N-PSDB; AAH43472.

XX

PT (R)-2-octanol dehydrogenase for producing intermediates for HMG-CoA

PT reductase inhibitors or D-carnitine.

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PS Claim 9; Page 83-85; 97pp; Japanese.

XX

CC This sequence represents (R)-2-octanol dehydrogenase which has the
 CC following characteristics: (1) produces ketones by oxidizing alcohol
 CC using beta-NAD as a co-enzyme; and produces alcohols by reducing ketones
 CC using beta-NADH as a co-enzyme; and (2) preferentially oxidizes the
 CC optical isomer (R)-2-octanol; and reduces 4-haloacetoacetate ester to
 CC produce (S)-4-halo-3- hydroxybutyrate ester. (S)-4-halo-3-hydroxybutyrate
 CC esters are useful as intermediates for HMG-CoA reductase inhibitors or D-
 CC carnitine. (R)-propoxybenzene derivatives are particularly useful as
 CC intermediates for optical isomers of ofloxane ((S)-(-)-9-fluoro-3-methyl-
 CC 10-(4-methyl-1- piperaziny)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4)
 CC benzoxadin- 6-carboxylic acid)

XX

SQ Sequence 254 AA;

Query Match 100.0%; Score 1298; DB 4; Length 254;

Best Local Similarity 100.0%; Pred. No. 2.9e-119;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSYNFHNKVAVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETTVVALKAQNLNTD 60

```

Db      1 MSYNFHNKVAVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETVVALKAQNLNTD 60
Qy      61 NLHYVQADSSKEEDNKKLISETLATFGGLDIVCANAGIGKFAPTHETPPFDVWKKVIAVNL 120
Db      61 NLHYVQADSSKEEDNKKLISETLATFGGLDIVCANAGIGKFAPTHETPPFDVWKKVIAVNL 120
Qy     121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAGGVKLLTQTLALEYA 180
Db     121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAGGVKLLTQTLALEYA 180
Qy     181 SHGIRVNSVNPGYISTPLIDEVPKERLDKLVSLHPIGRLGRPEEVADAVAFLCSQEATFI 240
Db     181 SHGIRVNSVNPGYISTPLIDEVPKERLDKLVSLHPIGRLGRPEEVADAVAFLCSQEATFI 240
Qy     241 NGVSLPVDGGGYTAQ 254
Db     241 NGVSLPVDGGGYTAQ 254

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RESULT 2

AAB49773

ID AAB49773 standard; protein; 254 AA.

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AC AAB49773;

XX

DT 23-APR-2001 (first entry)

XX

DE Protein with acetylpyridine derivative reducing action.

XX

KW Optically-active pyridineethanol derivative; asymmetric reduction.

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OS Candida maris.

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PN WO200105996-A1.

XX

PD 25-JAN-2001.

XX

PF 28-JUN-2000; 2000WO-JP004237.

XX

PR 21-JUL-1999; 99JP-00206503.

XX

PA (KANF) KANEKA CORP.

XX

PI Kawano S, Horikawa M, Yasohara Y, Hasegawa J;

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DR WPI; 2001-159546/16.

DR N-PSDB; AAF29375, AAF29376.

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PT Efficient, high-yielding preparation of optically-active pyridineethanol
PT derivatives by stereoselectively reducing acetylpyridine derivatives e.g.
PT with enzyme having asymmetric reduction activity, for pharmaceutical
PT intermediates.

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PS Claim 14; Fig 1; 76pp; Japanese.

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CC This invention relates to a process for producing optically-active

pyridineethanol derivatives by stereoselectively reducing acetylpyridine derivatives with an enzyme or enzyme source having asymmetric reduction activity. The process is efficient and high yielding to give R and S isomers by suitable manipulation. The method is for the preparation of optically-active pyridineethanol derivatives by stereoselectively reducing acetylpyridine derivatives, and also similarly for their polycyclic analogues, for use as pharmaceutical and agrochemical intermediates, as well as in fine chemical production. The present sequence represents the amino acid sequence of the enzyme used in the process which has acetylpyridine derivative reducing action

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SQ Sequence 254 AA;

Query Match 72.7%; Score 944; DB 4; Length 254;
 Best Local Similarity 69.7%; Pred. No. 2.4e-84;
 Matches 177; Conservative 36; Mismatches 41; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | MSYNFHNKVAVVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETVVALKAQNLNTD | 60 |
| | | : : : : : : | |
| Db | 1 | MSYNFANKVLIIVTGGLSGIGLAVAKKFLQLGAKVTISDISATEKYNTVVGEFKTEGIDVK | 60 |
| Qy | 61 | NLHYVQADSSKEEDNKKLISSETLATFGGLDIVCANAGIGKFAPTHETPFDVWKKVIAVNL | 120 |
| | | : : : : : : : : | |
| Db | 61 | NVQYIQADASKEADNEKLISSETLSAFGLDLDYVCANAGIATFTQTDDISYDVWRKVTSINL | 120 |
| Qy | 121 | NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAGGVKLLTQTLALEYA | 180 |
| | | : : : : : : : : | |
| Db | 121 | DGVFMLDKLAAQYFLSKNKPGAIVNMGSIHSHYVAAPGLSHYGAAGGGLKLLTQTMALAYEY | 180 |
| Qy | 181 | SHGIRVNSVNPGYISTPLIDEVPKERLDKLVSLHPIGRLGRPEEVADAVAFLCSQEATFI | 240 |
| | | : : : : : : | |
| Db | 181 | AKGIRVNSVNPGYIKTPLLDICPKEHMDYLITQHPIGRLGKPEEIASAVAFLCSDEATFI | 240 |
| Qy | 241 | NGVSLPVDGGYTAQ | 254 |
| | | : : | |
| Db | 241 | NGISLLVDGGYTAR | 254 |

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

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SUMMARIES

| Result No. | % | | Query Match Length | DB | ID | Description |
|---------------|-------|-------|-----------------------|----|----------------------|-------------------|
| | Score | Match | | | | |
| 1 | 1298 | 100.0 | 254 | 2 | US-09-978-758-2 | Sequence 2, Appli |
| 2 | 586.5 | 45.2 | 257 | 2 | US-09-543-681A-6362 | Sequence 6362, Ap |
| 3 | 503.5 | 38.8 | 309 | 2 | US-09-248-796A-16823 | Sequence 16823, A |
| 4 | 494.5 | 38.1 | 261 | 2 | US-09-468-738A-29 | Sequence 29, Appl |
| 5 | 494.5 | 38.1 | 261 | 2 | US-09-940-019-29 | Sequence 29, Appl |
| 6 | 494.5 | 38.1 | 261 | 2 | US-09-940-037A-29 | Sequence 29, Appl |
| 7 | 494.5 | 38.1 | 261 | 2 | US-09-305-390-18 | Sequence 18, Appl |
| 8 | 477.5 | 36.8 | 263 | 2 | US-09-710-279-204 | Sequence 204, App |
| 9 | 472.5 | 36.4 | 267 | 2 | US-09-134-001C-5042 | Sequence 5042, Ap |
| 10 | 470.5 | 36.2 | 251 | 2 | US-09-648-004-20 | Sequence 20, Appl |
| 11 | 470.5 | 36.2 | 251 | 2 | US-10-272-419-20 | Sequence 20, Appl |
| 12 | 453.5 | 34.9 | 261 | 2 | US-10-004-115B-36 | Sequence 36, Appl |
| 13 | 440 | 33.9 | 252 | 2 | US-08-822-322-8 | Sequence 8, Appli |
| 14 | 440 | 33.9 | 252 | 2 | US-09-466-109-8 | Sequence 8, Appli |
| 15 | 425 | 32.7 | 277 | 2 | US-09-543-681A-8037 | Sequence 8037, Ap |

Database : UniProt_05.80:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------------|--------------------|
| | | Match | Length | | | |
| 1 | 619.5 | 47.7 | 247 | 2 | Q81AU6_BACCR | Q81au6 bacillus ce |
| 2 | 577 | 44.5 | 246 | 2 | Q8G0H2_BRUSU | Q8g0h2 brucella su |
| 3 | 511.5 | 39.4 | 262 | 2 | Q5A1C0_CANAL | Q5a1c0 candida alb |
| 4 | 504.5 | 38.9 | 262 | 2 | Q5FK32_LACAC | Q5fk32 lactobacill |
| 5 | 494.5 | 38.1 | 261 | 1 | DHG_BACSU | P12310 bacillus su |
| 6 | 491.5 | 37.9 | 261 | 1 | DHGA_BACME | P10528 bacillus me |
| 7 | 490 | 37.8 | 244 | 2 | Q8ELC2_OCEIH | Q8elc2 oceanobacil |
| 8 | 488.5 | 37.6 | 261 | 1 | DHG4_BACME | P39485 bacillus me |
| 9 | 485.5 | 37.4 | 261 | 2 | Q632X4_BACCZ | Q632x4 bacillus ce |
| 10 | 484.5 | 37.3 | 261 | 2 | Q81KM8_BACAN | Q81km8 bacillus an |
| 11 | 482.5 | 37.2 | 261 | 1 | DHG3_BACME | P39484 bacillus me |
| 12 | 478.5 | 36.9 | 261 | 2 | Q4MVK1_BACCE | Q4mvk1 bacillus ce |
| 13 | 478.5 | 36.9 | 263 | 2 | Q5HLZ1_STAEQ | Q5hlz1 staphylococ |
| 14 | 477.5 | 36.8 | 261 | 1 | DHG2_BACME | P39483 bacillus me |
| 15 | 477.5 | 36.8 | 261 | 2 | Q6HCG4_BACHK | Q6hcg4 bacillus th |
| 16 | 477.5 | 36.8 | 261 | 2 | Q9F2A6_BACLI | Q9f2a6 bacillus li |
| 17 | 477.5 | 36.8 | 261 | 2 | Q65HM4_BACLD | Q65hm4 bacillus li |
| 18 | 474.5 | 36.6 | 261 | 2 | Q5BMD7_BACME | Q5bmd7 bacillus me |
| 19 | 473.5 | 36.5 | 259 | 2 | Q831W5_ENTFA | Q831w5 enterococcu |
| 20 | 473.5 | 36.5 | 261 | 2 | Q5BMD8_BACME | Q5bmd8 bacillus me |

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

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SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 494.5 | 38.1 | 261 | 2 | D69629 | glucose 1-dehydrog |
| 2 | 491.5 | 37.9 | 261 | 1 | S00812 | glucose 1-dehydrog |
| 3 | 488.5 | 37.6 | 261 | 2 | I40225 | glucose 1-dehydrog |
| 4 | 482.5 | 37.2 | 261 | 2 | I40224 | glucose 1-dehydrog |
| 5 | 477.5 | 36.8 | 261 | 2 | I39853 | glucose 1-dehydrog |
| 6 | 471.5 | 36.3 | 255 | 1 | S39737 | glucose 1-dehydrog |
| 7 | 455.5 | 35.1 | 261 | 2 | A33528 | glucose 1-dehydrog |
| 8 | 454.5 | 35.0 | 261 | 2 | JS0385 | glucose 1-dehydrog |
| 9 | 448 | 34.5 | 262 | 2 | S02299 | glucose 1-dehydrog |
| 10 | 448 | 34.5 | 272 | 2 | AG3359 | glucose 1-dehydrog |
| 11 | 446.5 | 34.4 | 263 | 2 | S01227 | glucose 1-dehydrog |
| 12 | 422.5 | 32.6 | 255 | 2 | G82644 | 2,5-dichloro-2,5-c |
| 13 | 420.5 | 32.4 | 258 | 2 | G69755 | glucose 1-dehydrog |
| 14 | 418.5 | 32.2 | 269 | 2 | AE2285 | glucose 1-dehydrog |
| 15 | 413.5 | 31.9 | 250 | 1 | S47054 | probable dehydroge |
| 16 | 404.5 | 31.2 | 251 | 2 | G72389 | oxidoreductase, sh |
| 17 | 396 | 30.5 | 246 | 2 | A69621 | 3-oxoacyl-[acyl-ca |
| 18 | 395.5 | 30.5 | 245 | 2 | AE3517 | 3-oxoacyl-(acyl-ca |
| 19 | 393 | 30.3 | 257 | 2 | A72395 | oxidoreductase, sh |
| 20 | 391.5 | 30.2 | 271 | 2 | AG3285 | 3-hydroxybutyrate |